



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96343

TO: Sarvamangala Devi
Location: cm1/7e15/7e12
Art Unit: 1645
Friday, June 20, 2003
Case Serial Number: 715876

From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

STIC-Biotech/ChemLib

96343

From: STIC-ILL
Sent: Wednesday, June 11, 2003 9:57 AM
To: STIC-Biotech/ChemLib
Subject: FW: 09/715,876

RECEIVED

JUN 11 2003

(STIC)

-----Original Message-----

From: Devi, Sarvamangala
Sent: Wednesday, June 11, 2003 9:54 AM
To: STIC-ILL
Subject: 09/715,876

Beverly:

Would you please perform a sequence and an interference search for SEQ ID NO: 7 and SEQ ID NO: 8 in application SN 09/715,876?

Thank you.

S. DEVI, Ph.D.
AU 1645
CM1-7E15
Mailbox: CM1-7E12

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 6/11
Date Completed: 6/20
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____

SEARCH REQUEST FORM



STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 112253

To: Sarvamangala Devi
Location: CM17E157E12
Art Unit: 1645
Tuesday, January 20, 2004

Case Serial Number: 09/715876

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Shears, Beverly

112253

From: Devi, Sarvamangala
Sent: Thursday, January 15, 2004 3:05 PM
To: Shears, Beverly
Subject: 09/715,876

Beverly:

Please perform a sequence and an interference search for an N-terminal nucleic acid sequence comprising nucleotides 52 to 1296 of SEQ ID No.7 in application SN 09/715,876.

Thank.

S. DEVI, Ph.D.
AU 1645

STAFF USE ONLY

Date completed: 01-14-04
Searcher: Beverly e 2528
Terminal time: 23
Elapsed time: _____
CPU time: _____
Total time: 23
Number of Searches: _____
Number of Databases: _____

Search Site: STIC CM-1 Pre-S
Type of Search: N.A. Sequence A.A. Sequence Structure Bibliographic

Vendors: IG STN Dialog APS Geninfo SDC DARC/Questel Other (S.N.)

Result No.	Score	Query Match	Length	DB	ID	Description
1	100	100	100	100	100	100

No.	Score	Match	Length	DB	ID	Description
1	1245	100.0	3786	15	US-10-245-802-7	Sequence 7, Appl
2	1046.6	84.1	3813	15	US-10-245-802-15	Sequence 15, Appl
3	949	76.2	4383	15	US-10-245-802-21	Sequence 21, Appl
4	947.4	76.1	3360	15	US-10-245-802-11	Sequence 11, Appl
5	895	71.9	1404	15	US-10-245-802-9	Sequence 9, Appl
6	733.4	58.9	1407	15	US-10-245-802-13	Sequence 13, Appl
7	713.8	57.3	1404	15	US-10-245-802-23	Sequence 23, Appl
8	574.6	46.2	4332	15	US-10-245-802-17	Sequence 17, Appl
9	393.6	31.6	6897	15	US-10-245-802-19	Sequence 19, Appl
10	55.4	4.4	436	9	US-09-864-761-2885	Sequence 2885, Ap
11	49.4	4.0	7758	13	US-10-311-455-1075	Sequence 1075, Ap
12	48.8	3.9	684973	10	US-09-363-959-1	Sequence 1, Appl
13	45.4	3.6	8201	13	US-10-363-798-1	Sequence 1, Appl
14	45	3.6	2280	13	US-10-032-585-6880	Sequence 6880, Ap
15	44.8	3.6	4985	13	US-10-056-405-10	Sequence 10, Appl

ALIGNMENTS

181 ACTACTTCACAAACATCTGTGATTTTAA

Query Match	100.0%;	Score 1245;	DB 15;	Length 3786;
Best Local Similarity	100.0%;	Pred. No. 2.2e-270;		

	Matches	1245;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;											
Qy	1	AAGACAAT	CAC	TGGT	GTTTT	TG	ATAGT	TTTT	TAAT	TCA	TTA	ATC	TTG	TCA	AT	TG	TG	CT	TA	AT	60
Db	52	AAGACAAT	CAC	TGGT	GTTTT	TG	ATAGT	TTTT	TAAT	TCA	TTA	ATC	TTG	TCA	AT	TG	TG	CT	TA	AT	111
Qy	61	TATGCTTT	CA	AGGG	CC	AG	GAT	CC	CA	AT	CT	GGA	AT	GCT	GT	TT	TGG	TT	TGG	T	120
Db	112	TATGCTTT	CA	AGGG	CC	AG	GAT	CC	CA	AT	CT	GGA	AT	GCT	GT	TT	TGG	TT	TGG	T	171
Qy	121	GGTAC	CAG	TGC	CA	AT	CC	AGG	GAT	CA	TT	CA	CA	AT	TG	CA	TAT	G	CA	TG	180
Db	172	GGTAC	CAG	TGC	CA	AT	CC	AGG	GAT	CA	TT	CA	CA	AT	TG	CA	TAT	G	CA	TG	231
Qy	181	ACT	ACT	CT	CA	AA	CA	AT	CT	CT	GT	TG	AT	TT	AA	CT	TG	CC	GA	TG	240

|||||
232 ACTACTTCACAAACATCTGTTGATTTAACTGCGGATGTTGTTAAATATGCTACTTGTCAA 291
QY
241 TTTTATTTCTGGTGAAGAATTCACAACTTTTCTACATTAACATGCTACTGTGAACGCGT 300
Db
292 TTTTATTTCTGGTGAAGAATTCACAACTTTTCTACATTAACATGCTACTGTGAACGCGT 351
QY
301 TTGAATCATCATTAAGGCAATTTGGTACAGTTTACTTTTACCAATTTGCAATTTGCT 360
Db
352 TTGAATCATCATTAAGGCAATTTGGTACAGTTTACTTTTACCAATTTGCAATTTGCT 411
QY
361 GGAACAGGTTTCATCAATGATTTGGAAGATTTCAATGTTTTTACTGCTGGTACCAATACA 420
Db
412 GGAACAGGTTTCATCAATGATTTGGAAGATTTCAATGTTTTTACTGCTGGTACCAATACA 471
QY
421 GTACATTTAATGATGTTGATTAAGATATCTCAATTTGATTTGAGTTTGAAGAAGTCAAC 480
Db
472 GTACATTTAATGATGTTGATTAAGATATCTCAATTTGATTTGAGTTTGAAGAAGTCAAC 531
QY
481 GTTGATCCAAAGTGCAATTTGATGTTCTCCAGAGTTTATGCCAAGTCTCAATAGGTCA 540
Db
532 GTTGATCCAAAGTGCAATTTGATGTTCTCCAGAGTTTATGCCAAGTCTCAATAGGTCA 591
QY
541 ACTCTTTTGTGGCACCACCAATGTTGAAGATTTGATTAACATCTGTTGATTAACATG 600
Db
592 ACTCTTTTGTGGCACCACCAATGTTGAAGATTTGATTAACATCTGTTGATTAACATG 651
QY
601 AGTAGTAACGGTGAAGTCTGATTTGATGTTCTCAATTTGATTTGAGTTTGAAGAAGTCA 660
Db
652 AGTAGTAACGGTGAAGTCTGATTTGATGTTCTCAATTTGATTTGAGTTTGAAGAAGTCA 711
QY
661 TTAAATGATTTGGAATTTATCCGGTTTCAATCTGATCAATTTAGTTTACATAAACTTGTACA 720
Db
712 TTAAATGATTTGGAATTTATCCGGTTTCAATCTGATCAATTTAGTTTACATAAACTTGTACA 771
QY
721 TCTAATGGAATTCAGATTAATAATCAAAATGATGATCTGCTGGTTATCGTCCATTTATTTGAT 780
Db
772 TCTAATGGAATTCAGATTAATAATCAAAATGATGATCTGCTGGTTATCGTCCATTTATTTGAT 831
QY
781 GCTTATATTTCTGCTACAGATTTTACCAATATATCTTTTACGATATATCAATGATTTATCT 840
Db
832 GCTTATATTTCTGCTACAGATTTTACCAATATATCTTTTACGATATATCAATGATTTATCT 891
QY
841 TGTGCTGGCAGTCTGCTGCAAGTAAACCTTTTCACTTTAAGATGGAATGGAATCAAGAAT 900
Db
892 TGTGCTGGCAGTCTGCTGCAAGTAAACCTTTTCACTTTAAGATGGAATGGAATCAAGAAT 951
QY
901 AGTGATGCCGGATCTAAACGGTATTTGCTATTTGCTGCTAACAATAGAACAGTTACAGACGT 960
Db
952 AGTGATGCCGGATCTAAACGGTATTTGCTATTTGCTGCTAACAATAGAACAGTTACAGACGT 1011
QY
961 ACCACTGCTGCTACTTACTTTTACCAATTTCAATCCAAAGTGTGATAAACCAAAACAAATCGAA 1020
Db
1012 ACCACTGCTGCTACTTACTTTTACCAATTTCAATCCAAAGTGTGATAAACCAAAACAAATCGAA 1071
QY
1021 ATTTTGCACCTATTTCCAAACCTTACCATCAACATTTCAATGTTGGTGTGACTACTTCC 1080
Db
1072 ATTTTGCACCTATTTCCAAACCTTACCATCAACATTTCAATGTTGGTGTGACTACTTCC 1131
QY
1081 TATCTGCTAAGACTGCAACCAATTTGTTGGAACAGCTACTGTTATTTGTTGATGTCATAT 1140
Db
1132 TATCTGCTAAGACTGCAACCAATTTGTTGGAACAGCTACTGTTATTTGTTGATGTCATAT 1191
QY
1141 CATACTACCAACTGTTTACAGTGAATGACAGGACCAATCACTACCAACCAACTCGT 1200
Db
1192 CATACTACCAACTGTTTACAGTGAATGACAGGACCAATCACTACCAACCAACTCGT 1251
QY
1201 ACCAATCCAACTGATTCATTTGACACAGTGGTGGTACAAAGTTCCA 1245
Db
1252 ACCAATCCAACTGATTCATTTGACACAGTGGTGGTACAAAGTTCCA 1296

US-10-245-802-15
; Sequence 15, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 15
; LENGTH: 3813
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-245-802-15

Query Match 84.1%; Score 1046.6; DB 15; Length 3813;
Best Local Similarity 90.0%; Pred. No. 1.2e-225;
Matches 1121; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 1 AAGCAATCATCTGCTGTTTGTATGATTTTAAATTCATTAACCTTGTGCTCAATGCTGCTAAT 60
Db 52 AAGCGCATCACTGGTATTTTCAATAGTATTTGACTCATTAATGCTGCTCAATGCTGCTAAT 111
QY 61 TATGCTTTCAAGGCGCCAGGATACCAACTTGGATGCTGTTTGGGTTGGTCTTATAGAT 120
Db 112 TACGCTTTCAAGGCGCCAGGATACCAACTTGGATGCTGTTTGGGTTGGTCTTATAGAT 171
QY 121 GGTACAGTCCCAATCCAGGGGATACATTCATTAAGATATGCCATGCTGTTTAAATAT 180
Db 172 GGTACAGTCCCAATCCAGGGGATACATTCATTAAGATATGCCATGCTGTTTAAATAT 231
QY 181 ACTACTTCAAAACATCTGTTGATTTAACTGCGGATGCTGTTAAATATGCTACTTGTCAA 240
Db 232 ACTGCTTCCCAAAATCTGTTGATTTGACTGCGGATGCTGTTAAATATGCTACTTGTCAA 291
QY 241 TTTTATTTCTGGTGAAGAATTCACAACTTTTCTACATTAACATGCTGTTGAACGCGT 300
Db 292 TTTTATTTCTGGTGAAGAATTCACAACTTTTCTACATTAACATGCTGTTGAACGCGT 351
QY 301 TTGAATCATCATTAAGGCAATTTGGTACAGTTTACTTTTACCAATTTGCAATTTGCT 360
Db 352 TTGAATCATCATTAAGGCAATTTGGTACAGTTTACTTTTACCAATTTGCAATTTGCT 411
QY 361 GGAACAGGTTTCATCAATGATTTGGAAGATTTCAATGTTTTTACTGCTGGTACCAATACA 420
Db 412 GGAACAGGTTTCATCAATGATTTGGAAGATTTCAATGTTTTTACTGCTGGTACCAATACA 471
QY 421 GTACATTTAATGATGTTGATTAAGATATCTCAATTTGATTTGAGTTTGAAGAAGTCAAC 480
Db 472 GTACATTTAATGATGTTGATTAAGATATCTCAATTTGATTTGAGTTTGAAGAAGTCAAC 531
QY 481 GTTGATCCAAAGTGCAATTTGATGTTCTCCAGAGTTTATGCCAAGTCTCAATAGGTCA 540
Db 532 GTTGATCCAAAGTGCAATTTGATGTTCTCCAGAGTTTATGCCAAGTCTCAATAGGTCA 591
QY 541 ACTCTTTTGTGGCACCACCAATGTTGAAGATTTGATTAACATCTGTTGATTAACATG 600
Db 592 ACTCTTTTGTGGCACCACCAATGTTGAAGATTTGATTAACATCTGTTGATTAACATG 651
QY 601 AGTAGTAACGGTGAAGTCTGATTTGATGTTCTCAATTTGATTTGAGTTTGAAGAAGTCA 660
Db 652 AGTAGTAACGGTGAAGTCTGATTTGATGTTCTCAATTTGATTTGAGTTTGAAGAAGTCA 711
QY 661 TTAAATGATTTGGAATTTATCCGGTTTCAATCTGATCAATTTAGTTTACATAAACTTGTACA 720
Db 712 TTAAATGATTTGGAATTTATCCGGTTTCAATCTGATCAATTTAGTTTACATAAACTTGTACA 771
QY 721 TCTAATGGAATTCAGATTAATAATCAAAATGATGATCTGCTGGTTATCGTCCATTTATTTGAT 780

Db 772 TCTTTGGTATCTCTATCATHACAAGTTCCTCGCGGTTATCGTCAATTTATGAC 831
Qy 781 GCTTATATTTCTGCTACAGATGTTAAACCAATATATCTTTAGCATATACCAATGATATATCT 840
Db 832 GCTTATATTTCTCCCTCAGATAAACCAGTATCAATTTGCTGATATAAATAAGTATATCT 891
Qy 841 TGTGCTGGCAGTCTGCTGCAAGTAAACCTTTTCACTTTTAAAGATGGAAGTCAACAAGAT 900
Db 892 TGTGTTGATGATTTATGGCAACATGACCTTTTCACTTTTAAATGGAGTGGATATAGAAT 951
Qy 901 AGTGATGCCGGATCTAACGGTATTTGTCATTTGTTGCTACCACTAGACAGTTACAGACGT 960
Db 952 AGTGATGCCGGATCTAACGGTATTTGTCATTTGTTGCTACCACTAGACAGTTACAGACGT 1011
Qy 961 ACCACTGTGCTCACTACTTTTACCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCA 1020
Db 1012 ACCACTGTGCTCACTACTTTTACCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCA 1071
Qy 1021 ATTTTGCACCTTATTTCCACCACTACCATCACAACCTTCAATTTGTTGTTGTTGTTGTTGTT 1080
Db 1072 ATTTTGCACCTTATTTCCACCACTACCATCACAACCTTCAATTTGTTGTTGTTGTTGTTGTT 1131
Qy 1081 TATCTGACTAAGACTGACCAATTTGTTGAAACAGCTACTGTTATTTGTTGTTGTTGTTGTTGTT 1140
Db 1132 TATCTGACTAAGACTGACCAATTTGTTGAAACAGCTACTGTTATTTGTTGTTGTTGTTGTTGTT 1191
Qy 1141 CATACTACCACTGTTTACCACTGAAATGGACAGGAACCAATCACTACCACTGTTGTTGTTGTTGTT 1200
Db 1192 CATACTACCACTGTTTACCACTGAAATGGACAGGAACCAATTAAGATGACTACCACTGTTGTT 1251
Qy 1201 ACCAATCCAACTGATTTCAATTTGACACAGTGGTGGTACAAAGTTCCA 1245
Db 1252 ACCAATCCAACTGATTTCAATTTGACACAGTGGTGGTACAAAGTTCCA 1296

RESULT 3

US-10-245-802-21
; Sequence 21, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 4383
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-245-802-21

Query Match 76.2%; Score 949; DB 15; Length 4383;
Best Local Similarity 85.1%; Pred. No. 1.3e-203;
Matches 1060; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

Qy 1 AAGACAATCAGTGGTGTGTTTGTATAGTTTAAATTCATTAATCTGTTGTCATGCTGCTAAT 60
Db 748 AAGACAATCAGTGGTGTGTTTCAACAGTGTAAATTCATTAATCTGTTGTCATGCTGCTAAT 807
Qy 61 TATGCTTTCAAGGCGCAGGATACCACTGGAATGCTGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGT 120
Db 808 TATCAATTAAGGAGCCAGGACCCCACTTGAATGCTGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGT 867
Qy 121 GGTACAGTGCCAAATCCAGGGGATACATTCATATTAATATATGCAATGCTGTTGTTTAAATAT 180
Db 868 GGTACTAGTGCAAGTCCGGAGATACATTCATTAATTAATGCAATGCTGTTGTTTAAATTT 927

Qy 181 ACTACTTCAAAAACATCTGTTGATTTAACTGCCGATGGTGTAAATATGCTACTTGTCAA 240
Db 928 ACTACTTCTCAAAACATCTGTTGATTTGATTCGTCTCATGGTGTAAATATGCTACTGTCAA 987
Qy 241 TTTTATTTCTGGTGAAGAATTCACAACTTTTCTACATTAACATGATGCTGTAACGACGT 300
Db 988 TTTGAGGAGGTTGAAGAATTTATGACCTTTTCTCATTAACATGATGCTGTAACGACAT 1047
Qy 301 TTGAATCATCCATTAAGGCATTTGGTACAGTTACTTTTACCAATTTGCAATTTCAATTTGCT 360
Db 1048 TTGACTCCATCTATTAAGGCTTTGGGTACTGTCACTTTACCACTTTGCAATTTCAATTTGCT 1107
Qy 361 GGAAACAGGTTTCACTCAACTGATTTGGAAGATTTCTAAATGTTTACTTGTGCTGTTACCAATACA 420
Db 1108 GGAACTGGTCTTCTGTTGATTTTGAAGAATTTCTAAATGTTTACTTGTGCTGTTACCAACA 1167
Qy 421 GTCAATTTTAAATGATGGTGATTAAGATATCTCAATTTGATTTGAGTTTGAAGAAGTCAACC 480
Db 1168 GTTACATTTTAAATGATGGTGGAAGAATCTTATTAATTTGATTTTGAAGAAGTCAAT 1227
Qy 481 GTTGATCCAAGTGCAATTTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATTAAGGTCA 540
Db 1228 GTCGATCCAAAAGGGTACTTAACTGATTTCCAGAGTTATACCAAGTCTCAACAAAGTCA 1287
Qy 541 ACTCTTTTGGTGGCACCAATGTAAGTGAAGTGTACATCTGTTGACAAATGCGGTTCTCC 600
Db 1288 ACTCTTTTGGTGGCACCAATGTAAGTGAAGTGTACATCTGTTGACAAATGCGGTTCTCC 1347
Qy 601 AGTAGTACGGTACGTTGCTTATGATTTGCTCAATATTTCAATTTGATTTGATTTGATTTGATTTG 660
Db 1348 AACCTTATGTTGATGTTCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1407
Qy 661 TTAATGATTTGGAATTTATCCGGTTTTCATCTGAATCAATTTAGTTACATTAATACTTTGTACA 720
Db 1408 TTGAATGATTTGGAATTTATCCGGTTTTCATCTGAATCAATTTAGTTACATTAATACTTTGTACA 1467
Qy 721 TCTAATGGAATTCAGATTTAAATATCAAAATGATCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 780
Db 1468 TCTAATGGAATTCAGATTTAAATATCAAAATGATCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1527
Qy 781 GCTTATATTTCTGCTACAGATTTTAAACCAATATCTTTAGCATATACCAATGATTTATCT 840
Db 1528 GCTTATATTTCTGCTACAGATTTTAACTGCTACACCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1587
Qy 841 TGTGCTGCACTGCTGCTGCAAGTAAACCTTTTCACTTTTAAAGATGCACTGGATACAAAGAT 900
Db 1588 TGTGCTGCTGTTTATTTGGCAACGTGCACTTTTCACTTTAAGATGCACTGGATACAAAGAT 1647
Qy 901 AGTGATCCGATCTAAGGTTATTTGCTGATTTGCTGCTACCACTAGACAGTTTACAGACAGT 960
Db 1648 AGTGATCCGATCTAAGGTTATTTGCTGATTTGCTGCTACCACTAGACAGTTTACAGACAGT 1707
Qy 961 ACCACTGCTGCTACTTTTACCACTTCAATTTCAAGTGTGTTGATTAATAACCAAAACCAATCGAA 1020
Db 1708 ACTACCGCGGTGACCACTTACCACTTCAATTTCAAGTGTGTTGATTAATAACCAAAACCAATCGAA 1767
Qy 1021 ATTTTGAACCTATTTCCAACTACCACTACCACTTCAATTTCAATTTGTTGTTGTTGTTGTTGTTGTT 1080
Db 1768 ATTTTGAACCTATTTCCAACTACCACTACCACTTCAATTTCAATTTGTTGTTGTTGTTGTTGTTGTT 1827
Qy 1081 TATCTGACTAGACGTCACCAATTTGGTGAACAGCTACTGTTATTTGTTGATTTGTTGATTTGTTGATTT 1140
Db 1828 TACCTGACCAAACTGACCAATTTGGGGAACCTGCTACTGTTTATTTGTTGATTTATTTCCATAT 1887
Qy 1141 CATACTACCACTGTTTACCAGTGAATGGACAGGAACCAATCACTTACCACCACTCACTCGT 1200
Db 1888 CACACTACCACTGTTTACCAGTGAATGGACAGGAACCAATCACTTACCACCACTCACTCGT 1947
Qy 1201 ACCAATCCAACTGATTTCAATTTGACACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1245
Db 1948 ACTAATCCAACTGATTTCAATTTGACACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1992

Db 178 AGTGCAAATCCAGGAGACACATTCACATTTGAATATGCCATGTGTTTAAATTTATTACC 237

RESULT 8
US-10-245-802-17
; Sequence 17, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 4332
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-245-802-17

Query Match 46.2%; Score 574.6; DB 15; Length 4332;
Best Local Similarity 66.8%; Pred. No. 3.5e-119; Indels 6; Gaps 1;
Matches 836; Conservative 0; Mismatches 409;

QY 1 AAGACAATCACTGGTGTGTTTGTAGTATTTTAAATTCATTAACTTGGTCCAAATGCTGCTAAT 60
DB 55 AAAAATATATCGGGAGTTTTCAGAGTTTTCAGACTCATTTGACCTATATCTAATACTGTTAAAC 114
QY 61 TATGCTTCAAAAGGCGCCGATACCACTTGAATGCTGTTTGGTGGTCTTATAGT 120
DB 115 TACCCATATGCGGGTCTGCTGTTATCAACATGAGCTGCTGTTTGGTGGAGCTGGAC 174
QY 121 GGTACCACTAGTCCAGGGGATACATTCACATTCGAATATGCGATGCTGTTTAAATAT 180
DB 175 GGAACACTAGTATCCAGGTGATACATTTACATTTGTCATGCTGCTGGTTTCAATTT 234
QY 181 ACTACTTCAAAACATCTGTGTGTTTAACTGCGATGGTGTAAATATGCTACTGTCAA 240
DB 235 ATTACACACAAACTTCAGTAGACTTAACTGCTAAATGGTGTCAAGTATGCAACATGACT 294
QY 241 TTTTATCTGGTGAAGAAATTCACACTTTTCTACATTAACATGACTGCTGACGAGCT 300
DB 295 TTCATGCGAGGGAACATTTACTCTTTTCAAGTATGAGTTGTGTAGTAAATAATGGG 354
QY 301 TTGAATCATCCATTAAAGGCAATTTGGTACAGTTTACTTTTACCAATTCGATTTCAATGTTGT 360
DB 355 CTATCTTCAAAATATCAGAGGTTTGTACCGTACGGCTACCAATTTCAATTCATGTTGGT 414
QY 361 GGAACAGTTTCATCAACTGATTTGGAAGATTCATAATGTTTACTGCTGGTACCAATACA 420
DB 415 GGAACGTTTCATCTGTCACATTCGAATTCGAAGTTTCAAGTGTTCACCTGCTGGAACGACCT 474
QY 421 GTCAATTTAATGATGCTGATGAAGATATCTCAATTTGATGTTGAGTTGGAAGTCAACC 480
DB 475 GTAACATTTACAGCGCGCATCAAAATTTCTACTACAGTCAATTTCCCTAAGACTCCA 534
QY 481 GTTATPCCAGTGCATATTTGTATGCTTCCAGAGTTTATGCGATGCTCAATAGGTGACA 540
DB 535 CAATCATCTAGTAGCTGTTGTTATTTTCGAGGGTTATTTCCAGTCTTGATTAATATCT 594
QY 541 ACTCTTTTGTGGCACCACAAATGTAAGTGTGTTACACATCTGGTAAATGCGGTTCTCC 600
DB 595 AGTCTGTTGTTGCTTCTCAGTGTACTGCTGGATATGCAATCGGTGCTGCGATTTTCA 654
QY 601 AGTAGTAACGGTGAAGTCTGATTTGATGCTCAATATTCATATTTGGTATCAAAAGGA 660
DB 655 GCAACAAAAGATGATGTGCAATTTGATTTGTTCTACTATACATGTGGGAATAACAAATGT 714
QY 661 TTAATATGATTTGAAATTTATCCGGTTTCTCATCTGAATCATTTAGTTTACATAAACTTGTACA 720

DB 715 TTCAATAGTTGGATATATGCGAGTATCATCAGAAATCAATTTTCTTACACCAAACTGTGACA 774
QY 721 TCTAATGGAATTCAGATTAAATATCAAAATGATACCTGCTGGTTATCGTCCATTTATTTGAT 780
DB 775 CCAAAACAGTTTATTTATTTACTTATGAAATGTTCTCGCAGGTTATCGTCCATTTATTTGAT 834
QY 781 GCTT-----ATATTTCTGCTACAGATGTTAAACCATATATATTTAGCATATACCAATGAT 834
DB 835 TCTTACGTGAAATAATCAGCAACACGAAATGGAAATTTAAATTTGAATTACACGAATATA 894
QY 835 TATACTTGTGCTGGCAGTGTCTGCAAAAGTAAACCTTTTCACTTTAAAGATGGAGCTGGATAC 894
DB 895 TACAATTTGATGATGGCAAAAGGGAATGATCTCTTATATATCTTTTGGACATCATAC 954
QY 895 AAGAATAGTAGTCCGGATCTAACGGTATTTGTCATTTGTTGCTACAACTAGAACAGTTTACA 954
DB 955 ACAATATAGTAGTCCAGGATCCAAATGGAGCTGCGGTAGTTGTTACTACGAGAACAGTCACT 1014
QY 955 GACAGTACCACCTGCTGTCTACTACTTTTACCATTCAATCCAAAGTGTTCATAAACCAAAACA 1014
DB 1015 GATTTCAACACAGCAATTTACCAATTTACCGTTTGGATCCCAAGTTGATATAAAACCAAAACC 1074
QY 1015 ATCGAAATTTTGCACCTATTCCAACTTACCACTTACCATCACAACCTTTCATATGTTGTTGACT 1074
DB 1075 ATGGAATATAGAACCCATCTCTACTACCATTTACTTCTTATATGTTGGATTTCT 1134
QY 1075 ACTTCTATPCTCACTAAGACTGCACCAATTTGGTGAACAGCTACTGTTTATTTGTTGATGG 1134
DB 1135 ACTTCACTTTCTACGAAGACTGCAACTATTTGGAGGAACAGCAACTGTTGTTGTTGATGTT 1194
QY 1135 CCATATCATCTACTACCACTGTTTACCAGTGAATGGAGGAACCAATCATCTACCACCA 1194
DB 1195 CCTTATCATCAACTTACCACTATCATCTAGTATATGAGCTGGATACCATCAAGT 1254
QY 1195 ACTCGTACCACCTCCAACTGATTTCAATTTGACACAGTGGTGGTCAAGTTCCA 1245
DB 1255 ACTTATCAAAATCCCCTGACTCGATCGATGATACAGTTGTTGTTACAGTTCCA 1305

RESULT 9
US-10-245-802-19
; Sequence 19, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 6897
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-245-802-19

Query Match 31.6%; Score 393.6; DB 15; Length 6897;
Best Local Similarity 57.8%; Pred. No. 2.9e-78;
Matches 721; Conservative 0; Mismatches 524; Indels 3; Gaps 1;

QY 1 AAGACAATCACTGGTGTGTTTGTAGTATTTTAAATTCATTAACTTGGTCCAAATGCTGCTAAT 60
DB 55 AAGAGATTAATGTTGTTTCAACCAATTCATTTGATATGTTCTTACATACACA 114
QY 61 TATGCTTTCAAGGCGCCAGGATACCAACTTGGAAATGCTGTTTGGTGGTCTTAGAT 120
DB 115 GCTCGATACGAAGAAATATCTACTCTTACCGCTAATGCTCAATTTGGAATGGGCTTTGGAT 174
QY 121 GGTACCACTGCCAATCCAGGGGATACATTCATTTGAATATGCCATGTGTGTTTAAATAT 180

1255 TACTTCGATGACATGACTTGGTCGATCTCTCTCATCTCTCTGAAAAATTCCA 1300

Query Match	4.4%	Score 55.4	DB 9	Length 436
Best Local Similarity	48.6%	Pred. No. 0.014		
Matches 152	Conservative 0	Mismatches 161	Indels 0	Gaps 0

Qy	914	CTAACGGTATTGTGCTACAACTAGAACAGTTACAGACAGTACCACTGCTGTCA	973
Db	68	CTATTGTCACTACTATTATACCACCTACCATTTAGTACTACCACCACCTATCATCACTACCATCA	127
Qy	974	CTACTTTACCAATCAATCCAGTGTTCATTAACCAACCAACAAATTCGAACCTTA	1033
Db	128	CTACTAATATCATATTACCACTACTATTACCAATACCACGACTATCATTTACTACTACTA	187
Qy	1034	TTCCAAACCACTACCACATCAACAACCTTCATATGTTGGTGTGACTACTTCTATCTGACTAAGA	1093
Db	188	CCACCTCCACCAATTACTACTACTAATGCTATCATTACTACTACTGCTTCTATAATTACTA	247
Qy	1094	CTGCACCAATTTGGTGAACAGCTACTGTTATTTGTTGATGTGCCATATCATATACACAA	1153
Db	248	CTCCTACTCCTACCAATTACTACTACTAGTAGTATACCACTTACTACTACTATCATTA	307
Qy	1154	CTGTTACCACTGAATGCAGACAGGAACATCACTACCACCAACTCGTACCACCAACTG	1213
Db	308	CTATTACCAACCACTTACTACTATCATTACTACTACTACCAACCACTTACTACTCTG	367
Qy	1214	ATTCAATTGACAC	1226
Db	368	CTGTCATTACTAC	380

RESULT 11	US-10-311-455-1075/c
Sequence 1075	Application US/10311455
Publication No.	US20030143606A1
GENERAL INFORMATION:	
APPLICANT:	OLEK, Alexander
APPLICANT:	PIEPENBROCK, Christian
APPLICANT:	BERLIN, Kurt
TITLE OF INVENTION:	Diagnosis of Diseases Associated with the Immune System by Determination of Cytosine Methylation
TITLE OF INVENTION:	cytosine methylation
FILE REFERENCE:	5013.1014
CURRENT APPLICATION NUMBER:	US/10/311,455
CURRENT FILING DATE:	2002-12-16
PRIOR APPLICATION NUMBER:	PCT/EP01/07537
PRIOR FILING DATE:	2001-07-02
PRIOR APPLICATION NUMBER:	DE 10032529.7
PRIOR FILING DATE:	2000-06-30
PRIOR APPLICATION NUMBER:	DE 10043826.1
PRIOR FILING DATE:	2000-09-01
NUMBER OF SEQ ID NOS:	2424
SEQ ID NO 1075	
LENGTH:	7758
TYPE:	DNA
ORGANISM:	Artificial Sequence
FEATURE:	
OTHER INFORMATION:	chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1075	

	Query Match	4.0%;	Score 49.4;	DB 13;	Length 7758;
	Best Local Similarity	47.7%;	Pred. No. 1.3;		
	Matches 177;	Conservative 0;	Mismatches 191;	Indels 3;	Gaps 1;
QY	859	CAAAAGTAAACCTTTCTACTTTTAAGATGCATGGGATACAAGAATAGTGAATCCGGATCTAAC	918		
DB	6240	CCAACTACCCCTCCTACTACACCAATATCTTCAACTACCCCTCTACTACCCAAATACT	6181		
QY	919	GGTATTGTCTATTTGGTACAACTAGAACAGTTACAGACAGTACCACTGCTGTCACTACT	978		
DB	6180	TCAACTACCCCTCCTCTCCTCCAAATACTTTTAACTACCCCTACTACTTCTCTAACTACT	6121		
QY	979	TTACCAATTCNATCCAAGTGTGTGATAAAACCAAAACAATCGAAATTTGGCAACCTATTCCA	1038		
DB	6120	TCAACTACACACCTACTACTCTTAAAAACCCCAACTACCCCTTCCTTAATACTCCAAATACT	6061		

Qy	1039	ACCACTACACATCAAACTTCATATGTTGGTGTGACTACTTCCTATCTGACTAAGACTGCA	1098
Db	6060	CCAACTACCCCTCTACTACTCCAAATACTTCAACTACCCCTCCTACTCTCCCAACTACT	6001
Qy	1099	CCAAATGGTGMAACGACTACTGTTATGTTGTGATGTGCCATATCATACTACTACCAACTGTT	1158
Db	6000	CCAAATACCCCTCTACTACTCCAAATACTTTAACTACCCCTCCTACTCTCCAAATACT	5941
Qy	1159	ACCACTGA---ATGGACAGGAAACAATCACTTACCACCACAACTCGTACCACCAACTGAT	1215
Db	5940	TCAACTACCCCATCTACTACTTAAAACTCTAACTACTTCTCCTACTAATCCAAATACT	5981
Qy	1216	TCAAATGACAC	1226
Db	5880	TCAACTACGCC	5870

RESULT 12
US-09-263-959-1
; Sequence 1, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WITH
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 684973 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-1

	Query Match	3.9%;	Score 48.8;	DB 10;	Length 684973;
	Best Local Similarity	46.2%;	Pred. No. 17;		
	Matches 241;	Conservative 0;	Mismatches 272;	Indels 9;	Gaps 2;
QY	704	ACACTAAACCTGTACATCTAATGGAATTCAGATTAAATATCAAAATGTACCTGCTGGTT	763		
DB	12574	ATACTACCACCTGGCACTACTGATCTGTTCCTATCAACACCACTCTTTCCCAAGTACTA	12633		
QY	764	ATCGTCCATTATTGATGCTTATATTTCTGTGTCACAGATGTAACCAATATACTTTTAGCAT	823		
DB	12634	CTAGTGTACACTAATACTACTGTGTTCTGTATACACTTCT---CCTTTCCCTACAAGTA	12699		
QY	824	ATACCAATGATTATCTTGTGTGGCAGTCGTCTCGAAAGTAAACCTTTTCACTTTTAAGAT	883		
DB	12691	CTACTAATGCTAGCACTAATGCTACTGTTCTCTATCAACACCACTCTTTCCCAACAAAGTA	13759		

Qy 884 GGACTGGATACAGAAATAGTATCGCGATCAAGCGTATTGTCAATTTGCTACAACTA 943
Db 12751 CTATTTGGTTTACAACTAATCTACTGTTCCCAATACAACTGCGCCCTTTCCCAAAATG 12810
Qy 944 GAACAGTTACAGACGTACCACTGCTG-----TCACCTACTTTACCAATTCAGTCAAGTG 997
Db 12811 CTAGTACTGTAGCACTAATCTACTGTTCTCTATACCAACACATGTTTTCGCAACAAGTA 12870
Qy 998 TTGATAAACCAAAACATCGAAATTTTGCACACTATTCCAAACCACTACCACTCAAACTT 1057
Db 12871 CTATTTGGTTTACAACTAATCTACTGTTCCGATACAACTGCGCCCTTTCCCAACAATA 12930
Qy 1058 CATATTTGGTGTGACTACTTCTCTATCTGATTAAGACGTGACCAATTTGGTGAACAGCTA 1117
Db 12931 CTACTACTGTAGCACTAATCTACTATTTCTCTATCAACACACACCTTTTTCGCAACAAGTA 12990
Qy 1118 CTGTTATTTGATGTGCGCATATCATACTACCAACACTGTTTACCAGTGAATGGACGAA 1177
Db 12991 CTATTTAGTTTACAACTAGTACTACTGTTCTCTGATACAACTGCTCTCTTCCCTACAAGTA 13050
Qy 1178 CAATCACTACCAACCAACTCTGATCAATCCAACTGATTCAA 1219
Db 13051 CTACTAGTGTAGCACTAATGCTACCCCTGTTCTCTATCACAA 13092

RESULT 13

US-10-363-798-1/c

; Sequence 1, Application US/10363798

; Publication No. US20030180280A1

; GENERAL INFORMATION:

; APPLICANT: Kong, Xiangyin

; APPLICANT: Xiao, Shangxi

; APPLICANT: Zhao, Guoping

; APPLICANT: Yu, Chuan

; APPLICANT: Hu, Landian

; TITLE OF INVENTION: METHOD OF DIAGNOSING AND TREATING DENTINOGENESIS IMPERFECTA

; TITLE OF INVENTION: TYPE II USING DENTIN SIALOPHOSPHOPROTEIN GENE AND CODED

; FILE OF INVENTION: PRODUCT THEREOF

; FILE REFERENCE: 9548.78USWO

; CURRENT APPLICATION NUMBER: US/10/363,798

; CURRENT FILING DATE: 2003-03-05

; PRIOR APPLICATION NUMBER: CN 00125042.6

; PRIOR FILING DATE: 2000-09-05

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 8201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-363-798-1

Query Match 3.6%; Score 45.4; DB 13; Length 8201;

Best Local Similarity 45.2%; Pred. No. 11;

Matches 166; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

Qy 184 ACTTCACAAACATCTGTTGATTAACTGCCGATGGTGTGTTAAATATGCTACTTGTCAATTT 243

Db 7119 ACTGCTATCACTGCTGCTACTGCTATCGCTGCTGTTGCTGCTGCTGCTGCTGCTGCT 7060

Qy 244 TATTCCTGGTGAAGAATTCACACTTTTCTACATTAACATGATGCTGTGACGACGCTTGG 303

Db 7059 ATTGCTACTCACTGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 7000

Qy 304 AAATCATCATTAAGGCATTTGGTACAGTACTTTTACCAATTTGCAATTCATGTTGTGGA 363

Db 6999 ATTACTGCTGCTCACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6940

Qy 364 ACAGGTTTCATCACTGATTGGAGATTTCTAAATGTTTTTACTGCTGGTACCAATACAGTC 423

Db 6939 GTTGTCACTACTATTACTGCTTCTACTGCTATCACTGCTGCTGCTGCTGCTGCTGCT 6880

Qy 424 ACATTTAATGATGGTGATGAAGATATCTCAATGATGTTGAGTGTGTTGAAAGTCAACCGTT 483

Db 6879 ACTGCTGTTGCTGCTATCACTGCTGCTACATACATGCTGCTGCTGCTGCTGCTGCTGCT 6820
Qy 484 GATCCAAAGTCATATTTGATGCTTCCAGAGTTATGCCAAGTTCCTCAATAGGTCACTCAACT 543
Db 6819 ACTGCTATTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6760
Qy 544 CTTTGTG 550
Db 6759 GTTGTG 6753

RESULT 14

US-10-032-585-6880

; Sequence 6880, Application US/10032585

; Publication No. US20030180953A1

; GENERAL INFORMATION:

; APPLICANT: Terry, Roemer D.

; APPLICANT: Bo, Jiang

; APPLICANT: Charles, Boone

; APPLICANT: Howard, Bussey

; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

; FILE REFERENCE: 10182-005-999

; CURRENT APPLICATION NUMBER: US/10/032,585

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 8000

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6880

; LENGTH: 2280

; TYPE: DNA

; ORGANISM: Candida albicans

US-10-032-585-6880

Query Match 3.6%; Score 45; DB 13; Length 2280;

Best Local Similarity 46.2%; Pred. No. 6.9;

Matches 222; Conservative 0; Mismatches 255; Indels 4; Gaps 2;

Qy 631 TCAATATTCATATTTGTTATGATACCAAGGATTAATGATGATGATGATGATGATGATGAT 687

Db 606 TCAATATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 665

Qy 688 TCTGAATCATTTAGTTACACTTAAACCTTTGTACATCTAATGGAATTCAGATTAATATCAAA 747

Db 666 TGAACCGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 725

Qy 748 AATGATCTGCTGTTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 806

Db 726 CCCGAAATTTTCCAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 785

Qy 807 CCAATATCTTTAGCATATACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 866

Db 786 TAAATTTGCTACTGGGATATATTAATTTCCAAATGAATTAATTAATTAATTAATTAATTAAT 845

Qy 867 ACCTTTTCACTTTAAGATGAGTGCATGATACAAAGATAGTATGATGATGATGATGATGATGAT 926

Db 846 AAATCTACTGTTTCCCATGCTCATATATAATAATAAAGAAAGTCCCTGGGTGAGG 905

Qy 927 CATTTGTTGCTAACTAGAACAGTTACAGACGATGATGATGATGATGATGATGATGATGATGAT 986

Db 906 AATGGAACAATACTATATCATTTAGTTGAAATAGTACTATTGAAGAAGAATTAACAAG 965

Qy 987 CAATCCAGTGTGATTAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1046

Db 966 AATTTCTTGGAAATGATATAAACAATTCATTTGAAATACCTTAAGTGTGTTGATTAACAT 1025

Qy 1047 CATCACAACTTCATATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1106

Db 1026 ACGGCAAAATTAACGAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1085

Qy 1107 T 1107

Db 1086 T 1086

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 17, 2004, 21:05:28 ; Search time 2967 Seconds
(without alignments)
10198.542 Million cell updates/sec

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Perfect score: 1245
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152338056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_hc.*

9: gb_estl.*

10: gb_est2.*

11: gb_hc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	155	12.4	1047	29	CNS07D6L
c 2	139.4	11.2	1011	29	CNS07DAY
c 3	121.2	9.7	1050	29	CNS07CMQ
c 4	82.6	6.6	525	29	BZ351620

c	5	80.4	6.5	735	29	CNS04NSM
c	6	80.2	6.4	843	29	BZ643413
	7	78.4	6.3	501	29	FR0048173
	8	77.6	6.2	513	29	BZ423698
	9	76.6	6.2	773	29	CNS01VTG
	10	75.8	6.1	480	29	BZ643398
	11	75.2	6.0	694	28	BH355163
	12	71.8	5.8	494	29	FR0048073
c	13	69.8	5.6	427	29	BZ423231
	14	69.6	5.6	350	28	BH879665
	15	69.6	5.6	989	29	CNS02HA4
	16	68.6	5.5	334	29	BZ614791
	17	68.4	5.5	395	29	BZ316940
	18	67.8	5.4	989	29	CC149236
	19	67.6	5.4	356	29	CC171914
	20	66.6	5.3	423	29	BZ309688
	21	66.6	5.3	933	28	AZ204694
c	22	65.8	5.3	530	28	AZ166409
	23	65.4	5.3	306	29	BZ375744
	24	64.8	5.2	311	29	BZ638753
	25	64.6	5.2	320	29	BZ314341
	26	64	5.1	305	29	BZ333772
	27	63.6	5.1	428	12	BQ036742
	28	63.4	5.1	621	28	AZ164800
	29	62.6	5.0	914	28	AZ205202
c	30	62.4	5.0	810	28	AZ199472
	31	62.2	5.0	788	28	AZ183942
	32	61.8	5.0	266	29	BZ313584
	33	61.6	4.9	287	29	BZ644508
	34	61.2	4.9	619	29	FR0047601
	35	60.8	4.9	550	29	FR0043207
	36	60.4	4.9	450	29	FR0025683
	37	59.6	4.8	320	29	CC167070
	38	59.4	4.8	798	10	BF936821
	39	59.2	4.8	575	29	BZ780846
	40	59	4.7	289	29	BZ332780
	41	58.8	4.7	271	29	BZ310041
	42	58.8	4.7	500	28	B67199
	43	58	4.7	559	29	BX121516
	44	58	4.7	824	28	AZ185454
	45	57.6	4.6	305	29	BZ621988

ALIGNMENTS

RESULT 1
CNS07D6L/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

1047 bp DNA linear GSS 08-JUL-2001
T7 end of clone BD0AA009H06 of library BD0AA from strain CBS 94 of
Candida tropicalis, genomic survey sequence.

AL440083.1 GI:12223494

GSS.

Candida tropicalis

Candida tropicalis

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; mitosporic Saccharomycetales; Candida.

1 (bases 1 to 1047)

Souciat J.L., Aigle, M., Artiguenave, P., Blandin, G.,

Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,

de-Montigny, J., Dujon, B., Durand, P., Lepingle, A., Llorente, B.,

Malpertuy, A., Neuvéglise, C., Ozier-Kalogeropoulos, O., Potier, S.,

Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,

Wincker, P., and Weissenbach, J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of

yeast species for molecular evolution studies

Yeast Lett. 487 (1), 3-12 (2000)

20584711

11152876

2 (bases 1 to 1047)

Blandin, G., Ozier-Kalogeropoulos, O., Wincker, P., Artiguenave, P. and

Dujon, B.

Qy 61 TATGCTTTCAAGGCGGAGGATACCCAACTTGGAAATGCTGTTTGGGTGCTCTTAGAT 120
 Db 730 TATGCATATCAAGGCTCTCAATATCCAAATGGAATGCCGTGCTGATTTGGTCTTAGAT 789
 Qy 121 GGTACCAAGTGCATCCAGGGATACATTCACATTTGAATATGCCATGCTGTTAAATAT 180
 Db 790 GGCACAACATCCCAAGGATACGTTTCACTTTGATCATGCCCTGTGCTTCAAGTTC 849
 Qy 181 ACTACTTCAACAACATCTGTTGATTTAACTGCCGATGGTGTAAATATGCTACTTGTCAA 240
 Db 850 ACTACGTYTGCAATCTCTGTTGGATCTGACTGCCAATGGKATGACATATGCCACATGTGAT 909
 Qy 241 TTTTAT-TCGTGGAGAAATTCACAACTTTTCTACATTAACATGATGTGAACAGCGC 299
 Db 910 CTTTCATGCCGGTGAAGAGTTTACTACTTACTAGTTTACGTTGACTGCTACTGTAVAGATTC 969
 Qy 300 TTTGAATATCATCCATTAAGGCATTTGGTA 328
 Db 970 GTTAAGTCTGTTTCAATGAAGCTATGGGATA 998

RESULT 3

CNS07CMQ/c
 LOCUS 1050 bp DNA linear GSS 08-JUL-2001
 DEFINITION T7 end of clone BD0AA004B02 of library BD0AA from strain CBS 94 of Candida tropicalis, genomic survey sequence.
 ACCESSION AL439368
 VERSION AL439368.1 GI:12222781
 KEYWORDS GSS.
 SOURCE Candida tropicalis
 ORGANISM Candida tropicalis
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
 1 (bases 1 to 1050)
 Souciet J.L., Aigle M., Artiguenave P., Blandin G., Bolotin-Fukuhara M., Bon E., Brottier P., Casaregola S., de-Montigny J., Dujon B., Durrens P., Lepingle A., Llorente B., Malpertuy A., Neuvéglise C., Ozier-Kalogeropoulos O., Potter S., Saurin W., Tekala P., Toffano-Nioche C., Wesolowski-Louvel M., Wincker P. and Weissenbach J.
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
 FEBS Lett. 487 (1), 3-12 (2000)
 11152876
 2 (bases 1 to 1050)
 Blandin G., Ozier-Kalogeropoulos O., Wincker P., Artiguenave P. and Dujon B.
 Genomic exploration of the hemiascomycetous yeasts: 16. Candida tropicalis
 FEBS Lett. 487 (1), 91-94 (2000)
 20584726
 11152891
 3 (bases 1 to 1050)
 Genoscope.
 Direct Submission
 Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: seqref.genoscope.cns.fr)
 This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source
 1..1050
 /organism="Candida tropicalis"

misc_feature
 complement (<7..>921)
 /notes="similar to O1368 [Agglutinin-like protein ALA1 precursor] [Candida albicans]"
 /evidence="not experimental"
 BASE COUNT 301 a 185 c 226 g 336 t 2 others
 ORIGIN

Query Match 9.7%; Score 121.2; DB 29; Length 1050;
 Best Local Similarity 61.3%; Pred. No. 7e-19;
 Matches 195; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
 Qy 928 ATTGTTGCTACACTAGACAGTTACAGACAGTACCACTGCTGCTCACTACTTTACCAATTC 987
 Db 972 ATTGAAATCATCTACTAGAACAGTTACAGAACCACTACCTACGTTACCACTTTTACCATT 913
 Qy 988 AATCCAAAGTGTGATAAAACCAAAACCAATCGAAATTTTGCACACTTATCCCAACCACTACC 1047
 Db 912 GATTGAGCTACCCAAAGACAGAACCATTTGAAATTTTAAACAATGCTTTTAAACAACA 853
 Qy 1048 ATCACAACCTTCATATGTTGGTGTGACTACTTCTCTGCTGACTAAGACTGCACCAATGGT 1107
 Db 852 ATAACAGGCTCATATGTGGTGTGTGACACACAGAAGTACAACTTCTCTTTTGTACTTGA 793
 Qy 1108 GAAACAGCTACTGTTATTTGTTGATGTCATATCACTACCACTGCTTACCACTGTTACCACTG 1167
 Db 792 GAGACTGCTACTGTATTTGTTGGAATGCCATACCATATATTACTACACAGTGCACAACTTT 733
 Qy 1168 TGACAGGAGCAATCACTACCACTGCTTACCACTGCTTACCACTGCTTACCACTGCTTACCA 1227
 Db 732 TGGATGAAGATACACTTCTACTTTGACAGTATTGTATCCATCAGAACTATTGATACT 673
 Qy 1228 GTGGTGTACAAAGTTCCA 1245
 Db 672 GTCGTTGTAATCATCCA 655

RESULT 4

BZ351620
 LOCUS 525 bp DNA linear GSS 12-NOV-2002
 DEFINITION hw04f06.g1 WGS-SbicolorF (JW107 adapted methyl filtered) Sorghum bicolor genomic clone hw04f06 5', genomic survey sequence.
 ACCESSION BZ351620
 VERSION BZ351620.1 GI:24915123
 KEYWORDS GSS.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 525)
 Rabinowicz P.D., O'Shaughnessy A.L., Balija V., Dedhia N., Katzenburger F., King L., Miller B., Muller S., Nascimento L., Zutavern T., Palmer L., McCombie W.R. and Martienssen R.A.
 Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
 Unpublished
 Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mccombie@cshl.org
 Plate: hw04 row: f column: 06
 Seq primer: -21M13UnivRev
 Class: shotgun
 High quality sequence stop: 525.
 Location/Qualifiers

FEATURES

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source
1. 525
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="hw04f06"
/lab_host="JM107 or DH5a"
/clone_lib="WGS-Sbicolorf (JM107 adapted methyl filtered)"
/note="Site 1: Xba I; Site 2: Xba I; The vector was digested with Xba I and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mpl9, .b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a."
BASE COUNT 155 a 176 c 20 g 174 t
ORIGIN
Query Match 6.6%; Score 82.6; DB 29; Length 525;
Best Local Similarity 47.4%; Pred. No. 1.8e-09;
Matches 247; Conservative 0; Mismatches 274; Indels 0; Gaps 0;

Qy 706 ACTAAACTTGTACATCAATGGAATTCAGATTAAATATCAAAATGACCTGCTGTTAT 765
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 5 ACTACTACTGTCTACTACTGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 64
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 766 CGTCCATTATTGATGCTTATTTCTGCTACAGATGTTAAACCAATATATCTTTAGCATAT 825
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 65 ACTACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 124
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 826 ACCAATGATATATCTTGTGCTGGCAGTGTGCGAAAGTAACCTTTCACTTTAAGATGG 885
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 125 ACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 184
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 886 ACTGATACAGATAGTAGGCGGATCTACGATTTGTCATTTGTTGCTACAACTAGA 945
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 185 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 244
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 946 ACAGTTACAGACGATACCACTGCTGCTCACTACTTTTACCAATTCAAATGTTGNTAAA 1005
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 245 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 304
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1006 ACCAAACAAATCGAAATTTTGGAACTTATTCACCACTACATCAATCTTATGTT 1065
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 305 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 364
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1066 GGTGTGACTCTTCTATCTGATGAAGACTGCACCAATTTGGTGAACAGCTACTGTTATT 1125
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 365 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 424
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1126 GTTGATGTGCCATATCATCTACCAACTGTTTACAGTGAATGGACAGCAATCACT 1185
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 425 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 484
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1186 ACCACCAACTCGTACCAATCCAACTGATTCATTTGACAC 1226
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 485 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 525
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
CNS04NSM/c 735 bp DNA linear GSS 01-SEP-2000
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 123M05 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL299119
VERSION AL299119.1 GI:8038260
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;

REFERENCE
1
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,P.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
10835645
REFERENCE
2
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Coataz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,P.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
20359837
1089143
1089143
3 (bases 1 to 735)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 151 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
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1. 735
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="123M05"
/clone_lib="G"
/note="Genoscope sequence ID : COBG123AG03UP1-end : T7"
BASE COUNT 242 a 45 c 223 g 197 t 28 others
ORIGIN
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Best Local Similarity 47.4%; Pred. No. 7e-09;
Matches 251; Conservative 6; Mismatches 272; Indels 1; Gaps 1;

Qy 699 TAGTTACATAAACCTTGTACATCTTAATGGAATTCAGATTAAATATCAAAATGACCTGC 758
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 530 TACTGCTAAACCTACTACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 471
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 759 TGGTTATCGCCATTATTGATGCTTATATTTCTGCTACAGATGTTAAACCAATATACCTTT 818
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 470 TGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 411
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 819 AGCATATACCAATGATTATATCTTGTGCTGCGAGTCTGTCGCAAAAGTAAACCTTTCACTTT 878
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 410 TGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 351
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 879 ARGATGAGCTGGATACAAGAATAGTAGTATGCGGATCTAAGCGGTATTTGTTGTTGCTAC 938
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 350 TACTACTACTTTTCTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 291
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 939 AACTAGACAGTTTACAGACAGTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 998
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 290 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 231
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 999 TGATMAAACCAAAACCAATCGAAATTTTGGCAACCTATTTCACCACTACTACCACTCCTC 1058
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 230 TACTGCTGCTACTACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 171
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1059 ATATGTTGGTGCTACTCTTCTCTATCTGATAGACGTCGACCAATTTGGTGAACAGCTAC 1118
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 170 TACTGCTGCTACTACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 111
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1119 TGTATTGTTGCTGCTGCTATCA-TACTACCACAACTGTTTACCAGTGAATGGACAGAA 1177

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QY	867	ACCTTTCATTTTAAGATGGCATGGAATACAGATACTGTGATCCCGGATCTAAACGGTATTGT	9236
DB	371	TACTACTACTACTATTACTTGCTACTACTCAAGAGTACTACTATTACTGTGCTACAACATC	430
QY	927	CATTGTGTCTACAACCTAGAACAGTTACAGACAGTACCACCTGTGCTCACTACTTTTACCATT	985
DB	431	TACTATTACTACTACTACAACTACTACTACTAAAACTACTACTATTACTACTACTACAAC	490
QY	987	CAATCCAAGTGTGTATATAAACCAAAACAATCGAAATTTTGGCAACCTATTTCACACCACTAC	1046
DB	491	TACTACTACTGTATTACTACTACTAAAACTACTACTATTACTACTACTATTACTATTAC	550
QY	1047	CATCACAACTTCATATGTTGGTGTGACTACTTCCCTACTCTGACTAAAGACTGCACCAATTGG	1106
DB	551	TACTACTACTACAAGTACTACTATTACTACTACTATTACTACTACTACAACCTACTACTAT	610
QY	1107	TGAACACAGCTACTGTTATTGTTGATGTGCCATATCATACTACCACAACTGTTTACCAGTGA	1166
DB	611	TACTACTACTACTTAGAAGCTACTACTACTACTACTAAAACTACTACTACTACTACTACTAC	670
QY	1167	ATGGACAGGAACAATCACTA 1186	
DB	671	TACTACCATGACTACTACTA 690	
RESULT 12	FR0048073	494 bp DNA linear GSS 05-JAN-2001	
LOCUS	DEFINITION	Fugu rubripes GSS sequence, clone 263K15bd8, genomic survey	
ACCESSION	AL444858		
VERSION	AL444858.1 GI:12052694		
KEYWORDS	GSS; genome survey sequence.		
SOURCE	Takifugu rubripes		
ORGANISM	Takifugu rubripes		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
AUTHORS	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neteleosteoi;		
TITLE	Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;		
JOURNAL	Tetraodontidae; Tetraodontidae; Takifugu.		
COMMENT	1 (bases 1 to 494)		
	Clark, M.S.		
	Direct Submission		
	Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource		
	Centre Hinxton, Cambridge, CB10 1SB. UK Email:		
	biohelp@hmp.mrc.ac.uk		
	Vector: pBluescript II KS		
	V type: phagemid		
	PRIMER: KS		
	DESCR:		
	One pass dye-terminator sequencing of BAC (pBelobACII) cloned		
	genomic sequence		
	The BACs can be obtained from http://www.incyte.com.		
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	/mol_type="genomic DNA"		
	/db_xref="taxon:31033"		
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	/clone_lib="BAC 263K15"		
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ORIGIN			
Query Match	5.8%; Score 71.8; DB 29; Length 494;		
Best Local Similarity	47.1%; Pred. No. 7.9e-07;		
Matches 220;	Conservative 0; Mismatches 247; Indels 0; Gaps 0		
QY	755	CTGCTGTTATCGTCCATTTTATGATGCTTATTTCTGCTACAGATGTTAACCAATATA	814
DB	25	CGGCTTCTACTACTACTAGTACTGCTGCTACTACTACGACTACGACTCTGCTGCTCGA	84
QY	815	CTTTAGCATATACCAATGATTATTTACTTGTGTCGAGTCGTCTGCAAGTAGTAACCTTTCA	874
DB	85	CTACTGCGACGACGACTGCTACTACTACTGCGGTGCTTCTACTGCTACTACTACGA	144

was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (x/y reads in M13mp19, b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a. "

BASE COUNT 112 a 110 c 13 g 115 t
ORIGIN
Query Match 5.6%; Score 69.6; DB 28; Length 350;
Best Local Similarity 52.4%; Pred. No. 2.4e-06;
Matches 153; Conservative 0; Mismatches 139; Indels 0; Gaps 0;
QY 921 TATTGTCAATGTTGTACAACTAGACAGTACAGACAGTACAGTGTGCTACTACTTT 980
DB 6 TACTACTACTTTTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 65
QY 981 ACCATTCAATCCAGTGTGATTAACCAACCAATCGAAATTTGCCACCTATTCCCAAC 1040
DB 66 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 125
QY 1041 CACTACCAATCAACATTCATATGTTGGTGTGACTACTTCTCTATCTGACTAAGACTGCACC 1100
DB 126 TACTAGGACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 185
QY 1101 AATTGTGAAACAGCTACTGTTATTGTTGATGGCCATATCATCTACTACCAACACTGTTAC 1160
DB 186 TACTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 245
QY 1161 CAGTGATGGCAGGAGCAATCATCTACCACTCCCACTCGTACCAATCCCACT 1212
DB 246 TACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 297

RESULT 15
CNS02HA4
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence 17 end of clone
139021 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL197365
AL197365.1 GI:7835515
VERSION
GSS; genome survey sequence.
KEYWORDS
SOURCE
ORGANISM
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE
1
AUTHORS
Roest Crolius H., Jaillon O., Dasilva C., Bouneau L., Fisher C.,
Bernot A., Fizames C., Wincker P., Brothier P., Quetier P.,
Saurin W. and Weissenbach J.
TITLE
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL
Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE
20296633
PUBMED
10835645

REFERENCE
2
AUTHORS
Roest Crolius H., Jaillon O., Dasilva C., Ozouf-Costaz C.,
Fizames C., Fischer C., Bouneau L., Billault A., Quetier P.,
Saurin W., Bernot A. and Weissenbach J.
TITLE
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL
Genome Res. 10 (7), 939-949 (2000)
MEDLINE
20359837
PUBMED
10899143

REFERENCE
3 (bases 1 to 989)
AUTHORS
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

COMMENT
This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source

1. 989
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="139021"
/clone_lib="G"
/note="Genoscope sequence ID : COAG139AH11P1-end : 17"
BASE COUNT 320 a 245 c 122 g 261 t 41 others
ORIGIN

Query Match 5.6%; Score 69.6; DB 29; Length 989;
Best Local Similarity 50.3%; Pred. No. 3.6e-06;
Matches 159; Conservative 4; Mismatches 153; Indels 0; Gaps 0;
QY 911 GATCTAACGGTATTGTTCATTGTTGCTACAACTAGACAGTGTGCTACTACTACTACTACTACTACT 970
DB 4 GATCCATCCTTAACGAGCGCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 63
QY 971 TCATCTACTTTTACCAATTCATTCCTCAAGTGTGATATAAAACCAAAATCGAAATTTGCAAC 1030
DB 64 CTACT 123
QY 1031 CTATTCGAACCACTACCAATTCATATGTTGGTGTGACTACTTCTCTACTACTACTACTACTACT 1090
DB 124 AAACCTACWACWACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 183
QY 1091 AGACTGCGACCAATTTGGTGAAACAGCTACTGTTATTGTTGATGTCATATCATCTACTACCA 1150
DB 184 CTAATACT 243
QY 1151 CAACTGTTTACCAGTGAATGGACAGGAAACATFCACTACCACCACTCGTACCAATCCAA 1210
DB 244 CTRCTACTACTACTACTACTACTACTACTGCTGCTAATACTACTACTACTACTACTACTACTACT 303
QY 1211 CTGATTCATTTGACAC 1226
DB 304 CTACT 319

Search completed: January 17, 2004, 23:33:50
Job time : 2972 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 17, 2004, 20:47:57 : Search time 89 Seconds
(without alignments)
6174.404 Million cell updates/sec

Title: US-09-715-876-7_COPY_52_1296
Perfect score: 1245
Sequence: 1 aagacaatacactgggtgtttt.....cagtggtgtacaagtcca 1245

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:
1: /cgm2_6/ptodata/1/ina/5A COMB.seq:
2: /cgm2_6/ptodata/1/ina/5B COMB.seq:
3: /cgm2_6/ptodata/1/ina/6A COMB.seq:
4: /cgm2_6/ptodata/1/ina/6B COMB.seq:
5: /cgm2_6/ptodata/1/ina/PTUS COMB.seq:
6: /cgm2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	82.4	6.6	100	1	US-08-145-705A-32
C 2	82.4	6.6	100	1	US-08-145-705A-34
C 3	76	6.1	100	1	US-08-145-705A-33
C 4	68	5.5	100	1	US-08-145-705A-36
C 5	61.4	4.9	5511	3	US-08-928-361B-2
C 6	61.4	4.9	5511	3	US-08-928-361B-2
C 7	61.4	4.9	7334	3	US-08-928-361B-1
C 8	61.4	4.9	7334	3	US-08-928-361B-1
C 9	57.2	4.6	100	1	US-08-145-705A-37
C 10	57	4.6	100	1	US-08-145-705A-35
C 11	55.2	4.4	5163	3	US-08-700-651-1
C 12	55.2	4.4	5163	3	US-08-928-361B-4
C 13	55.2	4.4	5163	3	US-08-588-995A-4
C 14	55.2	4.4	5318	3	US-08-700-651-2
C 15	55.2	4.4	5318	3	US-08-928-361B-3
C 16	55.2	4.4	5318	3	US-08-928-361B-3
C 17	50	4.0	1071	1	US-08-357-962-1
C 18	50	4.0	1071	1	US-08-878-106-1
C 19	48.6	3.9	425	1	US-08-357-962-5
C 20	48.6	3.9	425	1	US-08-878-106-5
C 21	42.8	3.4	951	4	US-09-328-475C-15
C 22	42.8	3.4	81001	4	US-09-750-580-1
C 23	42.6	3.4	740	3	US-09-451-117-1
C 24	42.6	3.4	740	4	US-09-888-655-1
C 25	42.2	3.4	4249	4	US-09-071-035-403
C 26	42.2	3.4	4359	4	US-09-071-035-401
C 27	41.4	3.3	2349	4	US-09-601-198-46

Sequence 1, Appli
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Sequence 6, Appli
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Sequence 21, Appli
Sequence 2732, Ap
Sequence 2128, Ap
Sequence 956, App
Sequence 1254, Ap
Sequence 1555, Ap
Sequence 1, Appli
Sequence 2131, Ap
Sequence 2843, Ap

28 41.2 3.3 6057 3 US-08-362-525-1
29 40.2 3.2 867 4 US-09-216-393B-340
30 40.2 3.2 867 4 US-09-216-393B-342
31 40.2 3.2 1397 4 US-09-216-393B-343
32 40.2 3.2 1397 4 US-09-216-393B-345
33 40 3.2 1023 1 US-08-032-393-1
34 40 3.2 1355 1 US-08-032-393-7
35 39.4 3.2 547 1 US-08-032-393-6
36 39.4 3.2 1664976 4 US-08-916-421B-1
37 38.8 3.1 5340 4 US-09-134-001C-2732
38 38.4 3.1 1674 4 US-09-328-352-2128
39 38 3.1 306 4 US-08-998-416-956
40 37.6 3.0 713 3 US-09-134-001C-1254
41 37.6 3.0 1674 4 US-08-916-421B-1
42 37.6 3.0 1664976 4 US-08-916-421B-1
43 37.6 3.0 2187 4 US-09-134-001C-2131
44 37.4 3.0 888 4 US-09-107-532A-2843
45 37

ALIGNMENTS

RESULT 1
US-08-145-705A-32/c
; Sequence 32, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: L. bberding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC PowerMate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: German P 42 36 708.5
; FILING DATE: October 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans

US-08-145-705A-36/c
; Sequence 36, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: L. Bieding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC PowerMate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: German P 42 36 708.5
; FILING DATE: October 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
; US-08-145-705A-36

Query Match 5.5%; Score 68; DB 1; Length 100;
Best Local Similarity 80.0%; Pred. No. 2.5e-08;
Matches 80; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 719 CATCTAATGCAATTCAGATTAAATATCAAAATGCTGCTGTTATCGTCAATTTATG 778
Db 100 CATCTAATGCAATTCATATACATATGAAATATCCCTGAGTTATCGTCAATTTATG 41
QY 779 ATGCTTATATTTCTGCTACAGATGTTAAACCAATATATCTT 818
Db 40 ACGTTTATGTAATCTGCTCGGATGTTAAACAGTATATTTT 1

RESULT 5
US-08-928-361B-2
; Sequence 2, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND

; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verny, Hana
; REGISTRATION/DOCKET NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480,76-1(HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5511 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-928-361B-2

Query Match 4.9%; Score 61.4; DB 3; Length 5511;
Best Local Similarity 50.9%; Pred. No. 4.2e-06;
Matches 146; Conservative 0; Mismatches 141; Indels 0; Gaps 0;
QY 933 TGCTACAACTAGAACAGTTTACAGACAGTACCACTGCTGTCAGTCTTACCAATTCATCC 992
Db 1035 TACTACTAGACACACACACACACAGTACTACTACTACTACTACTACTACTACTACTAC 1094
QY 993 AAGTGTTCATATAAACCAACCAATCGAAATTTTGCACCTATTCACCACTATTCACCACTAC 1052
Db 1095 CACGACAACTACACCAACCAACCACTACCAAGAAACCAACCAACCAACCAACCAAC 1154
QY 1053 AACTTCATATGTTGGTGTGACTACTTCTTCTGACTAGTGTGACCACTGTTACCAATGGTGAAC 1112
Db 1155 AACTTACTACTACTACACACACACACCACTACTACTACTACTACTACTACTACTACTACT 1214
QY 1113 AGCTACTGTTATGTTGTTGATGTGCTCATATCATACTACTACCACTGTTACCAATGGTGAAC 1172
Db 1215 TACT 1274
QY 1173 AGGACCAATCTACTACCACTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1219
Db 1275 AACCAACCAACCAACCAACCAACCACTACTACTACTACTACTACTACTACTACTACTACT 1321

RESULT 6
US-09-588-995A-2
; Sequence 2, Application US/09588995A
; Patent No. 6514697
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: BARNES, DEBRA A.
; APPLICANT: NELSON, RICHARD C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
; TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM

APPLICANT: NELSON, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT FILING DATE: 2000-06-06
PRIOR FILING DATE: 08/827,171
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR FILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 5163
TYPE: DNA
ORGANISM: Cryptosporidium parvum
US-09-588-995A-4

Query Match 4.4%; Score 55.2; DB 4; Length 5163;
Best Local Similarity 48.4%; Pred. No. 0.00015;
Matches 153; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 912 ATCTAACGGTATTGTCATTTGCTACAACTAGAACAGTTTACAGACAGTACCACTGCTGT 971
DB 591 AACTACTACTACTACTACTACTACGCAACCAACCAACCAACCAACCAACCAACCAAC 650
QY 972 CACTACTTTACCAATTCACCAAGTGTGATTAACCAACCAACCAACCAACCAACCAAC 1031
DB 651 AACTACTACTACTACTACTACTACGCAACCAACCAACCAACCAACCAACCAACCAAC 710
QY 1032 TATTCCAAACCACTTACCAATTCATATGTTGTTGATGTCCTACTTCTCTACTACTAA 1091
DB 711 AACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 770
QY 1092 GACTGCACCAATTTGTTGAAACAGTCTGTTATTTGTTGATGTCCTACTACTACTACT 1151
DB 771 TACTACTACCAACCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 830
QY 1152 AACTGTTACCAATTTGTTGAAACAGTCTGTTATTTGTTGATGTCCTACTACTACTACT 1211
DB 831 AACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 890
QY 1212 TGATTCAATTGACACA 1227
DB 891 CACAACCAACCAACA 906

RESULT 14
US-08-700-651-2
Sequence 2, Application US/08/700651B
Patent No. 6015882
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2

LENGTH: 5318
TYPE: DNA
ORGANISM: Cryptosporidium parvum
US-08-700-651-2

Query Match 4.4%; Score 55.2; DB 3; Length 5318;
Best Local Similarity 48.4%; Pred. No. 0.00015;
Matches 153; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 912 ATCTAACGGTATTGTCATTTGCTACAACTAGAACAGTTTACAGACAGTACCACTGCTGT 971
DB 592 AACTACTACTACTACTACTACTACGCAACCAACCAACCAACCAACCAACCAACCAAC 651
QY 972 CACTACTTTACCAATTCACCAAGTGTGATTAACCAACCAACCAACCAACCAACCAAC 1031
DB 652 AACTACTACTACTACTACTACTACGCAACCAACCAACCAACCAACCAACCAACCAAC 711
QY 1032 TATTCCAAACCACTTACCAATTCATATGTTGTTGATGTCCTACTTCTCTACTACTAA 1091
DB 712 AACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 771
QY 1092 GACTGCACCAATTTGTTGAAACAGTCTGTTATTTGTTGATGTCCTACTACTACTACT 1151
DB 772 TACTACTACCAACCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 831
QY 1152 AACTGTTACCAATTTGTTGAAACAGTCTGTTATTTGTTGATGTCCTACTACTACTACT 1211
DB 832 AACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 891
QY 1212 TGATTCAATTGACACA 1227
DB 892 CACAACCAACCAACA 907

RESULT 15
US-08-928-361B-3
Sequence 3, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verdy, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1 (HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

PD 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00666.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488999/53.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX Claim 1; SEQ ID No 2885; 530pp; English.
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 436 BP; 137 A; 144 C; 15 G; 140 T; 0 other;
Query Match 4.4%; Score 55.4; DB 22; Length 436;
Best Local Similarity 48.6%; Pred. No. 0.0019;
Matches 152; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
QY 914 CTAACGGTATGTCATGTTGCTACCACTAGAACAGTTACAGACAGTACCTGCTGCA 973
DB 68 CTATTGTCACACTATTACCACTTACCATTAGTACTACCACTATCATCTACCATCA 127
QY 974 CTACTTTACCATTCATCCAGTGTGATATAAACCAAAACAAATCGAAATTTGCAACCTA 1033
DB 128 CTACTTAATCTATCATCTACCTACTATTAATCCATGCTATCTACTACTACTACTA 187
QY 1034 TTCCAACTACCTACCACTTCAATCTATGTTGGTGTGACTACTTCTATCTGACTAAGA 1093
DB 188 CCACCTCCACCACTTACTACTACTATTAATGCTATCTACTACTACTACTACTACTA 247
QY 1094 CTGCAACAAATGGTGAACAGCTACTGTTATGTTGATGTGCCATATCATATCAACAA 1153
DB 308 CTATTACCACTACCACTTACTACTATCTACTACTACTACTACTACTACTACTACTA 307
QY 1214 ATTCAATTGACAC 1226
DB 368 CTGTCATTACTAC 380.
RESULT 14
ID AAK02925
XX AAK02925 standard; DNA; 436 BP.
XX AAK02925;
XX

DT 05-NOV-2001 (first entry)
XX Human brain expressed single exon probe SEQ ID NO: 2916.
DE
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
OS Homo. sapiens.
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00667.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX Example 4; SEQ ID NO: 2916; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX Sequence 436 BP; 137 A; 144 C; 15 G; 140 T; 0 other;
Query Match 4.4%; Score 55.4; DB 22; Length 436;
Best Local Similarity 48.6%; Pred. No. 0.0019;
Matches 152; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
QY 914 CTAACGGTATGTCATGTTGCTACCACTAGAACAGTTACAGACAGTACCTGCTGCA 973
DB 68 CTATTGTCACACTATTACCACTTACCATTAGTACTACCACTATCATCTACTACTA 127
QY 974 CTACTTTACCATTCATCCAGTGTGATATAAACCAAAACAAATCGAAATTTGCAACCTA 1033
DB 128 CTACTTAATCTATCATCTACCTACTATTAATCCATGCTATCTACTACTACTACTA 187
QY 1034 TTCCAACTACCTACCACTTCAATCTATGTTGGTGTGACTACTTCTATCTGACTAAGA 1093
DB 188 CCACCTCCACCACTTACTACTACTATTAATGCTATCTACTACTACTACTACTACTA 247
QY 1094 CTGCAACAAATGGTGAACAGCTACTGTTATGTTGATGTGCCATATCATATCAACAA 1153
DB 248 CTCTACTCTTACCACTTACTACTACTACTACTACTACTACTACTACTACTACTA 307
QY 1154 CTGTTACCACTGAAATGGACAGGAAACAAATCACTACCAACCACTCGTACCAATCACTG 1213
DB 308 CTATTACCACTACCACTTACTACTATCTACTACTACTACTACTACTACTACTACTG 367
QY 1214 ATTCAATTGACAC 1226
DB 368 CTGTCATTACTAC 380

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RESULT 15
AAK28369
ID AAK28369 standard; DNA; 436 BP.
XX
AC AAK28369;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 2926.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
FN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 2926; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 436 BP; 137 A; 144 C; 15 G; 140 T; 0 other;

Query Match 4.4%; Score 55.4; DB 22; Length 436;
Best Local Similarity 48.6%; Pred. No. 0.0019;
Matches 152; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 914 CTAACGGTATTTGCTATTGTTGCTACAACTAGAACAGTTACACAGTACAGTACCACTGCTGTCA 973
DB 68 TTTTGTGCTACTACTATACCACTACCACTATGACTACCACTATCATCATCACTACCATCA 127
QY 974 CTACTTTTACCATTCAATCCAACTGTTGATAAAACCAAAACAAATCGAAATTTTGCAACCTA 1033
DB 128 CTACTAATCTATCATTTACCACTACTATTTACCACTACCACTATCATCTACTACTACTA 187
QY 1034 TTCCAACCACTACCACTACCACTTCCATATGTTGGTGTGCTACTTCTCTATCTGACTAAGA 1093
DB 188 CCACCTCCACCACTACTACTACTATGCTATCATCTACTACTACTGCTTCTTATAATTA 247
QY 1094 CTGCACCAATTTGGTGAACAGTACTGTTATTTGTTGATGTGCGCATATCATACTACCACAA 1153
DB 248 CTCCTACTCTCCACCACTACTACTAGTAGTATCACCATTACTACTACTACTACTATCATTA 307
QY 1154 CTGTTTACCAGTGAATGGACAGGAAACAATCACTACCACTACCACTCGTACCAATCCAACTG 1213
DB 308 CTATTACCACCACTACTACTACTATCATCTACTACTACTACTACTACTACTACTACTCTG 367
```

QY 1214 ATTCAATTGACAC 1226
DB 368 CTGTCACTACTAC 380

Search completed: January 17, 2004, 21:22:32
Job time : 384 secs

52 to 1296 of SEQ ID NO.7

RESULT 1
YSAALS1
LOCUS YSAALS1 3786 bp DNA linear PLN 03-MAY-2000
DEFINITION Candida albicans agglutinin-like sequence (ALS1) gene, complete
cds.
ACCESSION L25902
VERSION L25902.1 GI:704426
KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE 1 (bases 1 to 3786)
AUTHORS Hoyer,L.L., Scherer,S., Shatzman,A.R. and Livi,G.P.
TITLE Candida albicans ALS1: domains related to a Saccharomyces

to have a

[illegible]